PAGE: 1   **RAW SEQUENCE LISTING**
PATENT APPLICATION *US/09/079,569*   DATE: 07/30/98
TIME: 10:19:28

INPUT SET: S3286.raw

1652

This Raw Listing contains the General
Information Section and up to the first 5 pages.

ENTERED

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 1                              SEQUENCE LISTING
 2
 3   (1)     General Information:
 4
 5        (i) APPLICANT: Boyle, William J.
 6
 7       (ii) TITLE OF INVENTION: OSTEOPROTEGERIN BINDING PROTEINS
 8
 9      (iii) NUMBER OF SEQUENCES: 7
10
11       (iv) CORRESPONDENCE ADDRESS:
12              (A) ADDRESSEE: Amgen Inc.
13              (B) STREET: 1840 Dehavilland Drive
14              (C) CITY: Thousand Oaks
15              (D) STATE: California
16              (E) COUNTRY: USA
17              (F) ZIP: 91230-1789
18
19        (v) COMPUTER READABLE FORM:
20              (A) MEDIUM TYPE: Floppy disk
21              (B) COMPUTER: IBM PC compatible
22              (C) OPERATING SYSTEM: PC-DOS/MS-DOS
23              (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
24
25       (vi) CURRENT APPLICATION DATA:
26              (A) APPLICATION NUMBER: 09/079,569
27              (B) FILING DATE:
28              (C) CLASSIFICATION:
29
30      (vii) PRIOR APPLICATION DATA:
31              (A) APPLICATION NUMBER:  08/842,842
32              (B) FILING DATE:
33
34     (viii) ATTORNEY/AGENT INFORMATION:
35              (A) NAME: Winter, Robert B.
36              (C) REFERENCE/DOCKET NUMBER: A-451
37
38
39   (2) INFORMATION FOR SEQ ID NO:1:
40
41        (i) SEQUENCE CHARACTERISTICS:
42              (A) LENGTH: 52 base pairs
43              (B) TYPE: nucleic acid
44              (C) STRANDEDNESS: single
45              (D) TOPOLOGY: linear
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47          (ii) MOLECULE TYPE: cDNA
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49
50
51
52          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
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54   GTTCTCCTCA TATGGATCCA AACCGTATTT CTGAAGACAG CACTCACTGC TT              52
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56   (2) INFORMATION FOR SEQ ID NO:2:
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58          (i) SEQUENCE CHARACTERISTICS:
59              (A) LENGTH: 37 base pairs
60              (B) TYPE: nucleic acid
61              (C) STRANDEDNESS: single
62              (D) TOPOLOGY: linear
63
64          (ii) MOLECULE TYPE: cDNA
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66
67
68
69          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
70
71   TACGCACTCC GCGGTTAGTC TATGTCCTGA ACTTTGA                                37
72
73   (2) INFORMATION FOR SEQ ID NO:3:
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75          (i) SEQUENCE CHARACTERISTICS:
76              (A) LENGTH: 53 base pairs
77              (B) TYPE: nucleic acid
78              (C) STRANDEDNESS: single
79              (D) TOPOLOGY: linear
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81          (ii) MOLECULE TYPE: cDNA
82
83
84
85
86          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
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88   GTTCTCCTCA TATGAAACCT GAAGCTCAAC CATTTGCACA CCTCACCATC AAT              53
89
90   (2) INFORMATION FOR SEQ ID NO:4:
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92          (i) SEQUENCE CHARACTERISTICS:
93              (A) LENGTH: 45 base pairs
94              (B) TYPE: nucleic acid
95              (C) STRANDEDNESS: single
96              (D) TOPOLOGY: linear
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98          (ii) MOLECULE TYPE: cDNA
99
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110             (A) LENGTH: 59 base pairs
111             (B) TYPE: nucleic acid
112             (C) STRANDEDNESS: single
113             (D) TOPOLOGY: linear
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115        (ii) MOLECULE TYPE: cDNA
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117
118
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120        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
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124    (2) INFORMATION FOR SEQ ID NO:6:
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127             (A) LENGTH: 2295 base pairs
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129             (C) STRANDEDNESS: single
130             (D) TOPOLOGY: linear
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132        (ii) MOLECULE TYPE: cDNA
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135        (ix) FEATURE:
136             (A) NAME/KEY: CDS
137             (B) LOCATION: 158..1105
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140        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
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142    GAGCTCGGAT CCACTACTCG ACCCACGCGT CCGGCCAGGA CCTCTGTGAA CCGGTCGGGG    60
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144    CGGGGGCCGC CTGGCCGGGA GTCTGCTCGG CGGTGGGTGG CCGAGGAAGG GAGAGAACGA   120
145
146    TCGCGGAGCA GGGCGCCCGA ACTCCGGGCG CCGCGCC ATG CGC CGG GCC AGC CGA    175
147                                            Met Arg Arg Ala Ser Arg
148                                             1                   5
149
150    GAC TAC GGC AAG TAC CTG CGC AGC TCG GAG GAG ATG GGC AGC GGC CCC    223
151    Asp Tyr Gly Lys Tyr Leu Arg Ser Ser Glu Glu Met Gly Ser Gly Pro
152              10                  15                  20
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154   GGC GTC CCA CAC GAG GGT CCG CTG CAC CCC GCG CCT TCT GCA CCG GCT        271
155   Gly Val Pro His Glu Gly Pro Leu His Pro Ala Pro Ser Ala Pro Ala
156        25                30            35
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158   CCG GCG CCG CCA CCC GCC GCC TCC CGC TCC ATG TTC CTG GCC CTC CTG        319
159   Pro Ala Pro Pro Pro Ala Ala Ser Arg Ser Met Phe Leu Ala Leu Leu
160        40                45            50
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162   GGG CTG GGA CTG GGC CAG GTG GTC TGC AGC ATC GCT CTG TTC CTG TAC        367
163   Gly Leu Gly Leu Gly Gln Val Val Cys Ser Ile Ala Leu Phe Leu Tyr
164   55                60                65                70
165
166   TTT CGA GCG CAG ATG GAT CCT AAC AGA ATA TCA GAA GAC AGC ACT CAC        415
167   Phe Arg Ala Gln Met Asp Pro Asn Arg Ile Ser Glu Asp Ser Thr His
168                75                80                85
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170   TGC TTT TAT AGA ATC CTG AGA CTC CAT GAA AAC GCA GGT TTG CAG GAC        463
171   Cys Phe Tyr Arg Ile Leu Arg Leu His Glu Asn Ala Gly Leu Gln Asp
172                90                95            100
173
174   TCG ACT CTG GAG AGT GAA GAC ACA CTA CCT GAC TCC TGC AGG AGG ATG        511
175   Ser Thr Leu Glu Ser Glu Asp Thr Leu Pro Asp Ser Cys Arg Arg Met
176        105               110               115
177
178   AAA CAA GCC TTT CAG GGG GCC GTG CAG AAG GAA CTG CAA CAC ATT GTG        559
179   Lys Gln Ala Phe Gln Gly Ala Val Gln Lys Glu Leu Gln His Ile Val
180        120               125               130
181
182   GGG CCA CAG CGC TTC TCA GGA GCT CCA GCT ATG ATG GAA GGC TCA TGG        607
183   Gly Pro Gln Arg Phe Ser Gly Ala Pro Ala Met Met Glu Gly Ser Trp
184   135               140               145               150
185
186   TTG GAT GTG GCC CAG CGA GGC AAG CCT GAG GCC CAG CCA TTT GCA CAC        655
187   Leu Asp Val Ala Gln Arg Gly Lys Pro Glu Ala Gln Pro Phe Ala His
188                155               160               165
189
190   CTC ACC ATC AAT GCT GCC AGC ATC CCA TCG GGT TCC CAT AAA GTC ACT        703
191   Leu Thr Ile Asn Ala Ala Ser Ile Pro Ser Gly Ser His Lys Val Thr
192                170               175               180
193
194   CTG TCC TCT TGG TAC CAC GAT CGA GGC TGG GCC AAG ATC TCT AAC ATG        751
195   Leu Ser Ser Trp Tyr His Asp Arg Gly Trp Ala Lys Ile Ser Asn Met
196        185               190               195
197
198   ACG TTA AGC AAC GGA AAA CTA AGG GTT AAC CAA GAT GGC TTC TAT TAC        799
199   Thr Leu Ser Asn Gly Lys Leu Arg Val Asn Gln Asp Gly Phe Tyr Tyr
200        200               205               210
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202   CTG TAC GCC AAC ATT TGC TTT CGG CAT CAT GAA ACA TCG GGA AGC GTA        847
203   Leu Tyr Ala Asn Ile Cys Phe Arg His His Glu Thr Ser Gly Ser Val
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210    AAA ATC CCA AGT TCT CAT AAC CTG ATG AAA GGA GGG AGC ACG AAA AAC      943
211    Lys Ile Pro Ser Ser His Asn Leu Met Lys Gly Gly Ser Thr Lys Asn
212                250                 255                 260
213
214    TGG TCG GGC AAT TCT GAA TTC CAC TTT TAT TCC ATA AAT GTT GGG GGA      991
215    Trp Ser Gly Asn Ser Glu Phe His Phe Tyr Ser Ile Asn Val Gly Gly
216            265                 270                 275
217
218    TTT TTC AAG CTC CGA GCT GGT GAA GAA ATT AGC ATT CAG GTG TCC AAC      1039
219    Phe Phe Lys Leu Arg Ala Gly Glu Glu Ile Ser Ile Gln Val Ser Asn
220        280                 285                 290
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222    CCT TCC CTG CTG GAT CCG GAT CAA GAT GCG ACG TAC TTT GGG GCT TTC      1087
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226    AAA GTT CAG GAC ATA GAC TGAGACTCAT TTCGTGGAAC ATTAGCATGG            1135
227    Lys Val Gln Asp Ile Asp
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230    ATGTCCTAGA TGTTTGGAAA CTTCTTAAAA AATGGATGAT GTCTATACAT GTGTAAGACT    1195
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232    ACTAAGAGAC ATGGCCCACG GTGTATGAAA CTCACAGCCC TCTCTCTTGA GCCTGTACAG    1255
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234    GTTGTGTATA TGTAAAGTCC ATAGGTGATG TTAGATTCAT GGTGATTACA CAACGGTTTT    1315
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236    ACAATTTTGT AATGATTTCC TAGAATTGAA CCAGATTGGG AGAGGTATTC CGATGCTTAT    1375
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238    GAAAAACTTA CACGTGAGCT ATGGAAGGGG GTCACAGTCT CTGGGTCTAA CCCCTGGACA    1435
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246    GTGTAATGTT TTCTGTGCAA AGTTTTGTAA ATTATATTTG TGCTATAGTA TTTGATTCAA    1675
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250    ACTGGTGCAC TTTGTAATTC CCCTGAAGGT ACTCGTAGCT AAGGGGGCAG AATACTGTTT    1795
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254    GTCAAAACTA TGCAAGCAAA ATAAATAAAT AAAAATAAAA TGAATACCTT GAATAATAAG    1915
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256    TAGGATGTTG GTCACCAGGT GCCTTTCAAA TTTAGAAGCT AATTGACTTT AGGAGCTGAC    1975
257
258    ATAGCCAAAA AGGATACATA ATAGGCTACT GAAATCTGTC AGGAGTATTT ATGCAATTAT    2035
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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION *US/09/079,569*

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